Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 0   expect: 10.000   wordsize: 11   Filter ☑   View option Standard
Masking character option X for protein, n for nucleotide ▼   Masking color option Black ▼
☐ Show CDS translation   Align

Sequence 1: lcl|1 SEQ ID NO:101 from Pompejus et al.
Length = 861 (1 .. 861)

Sequence 2: gi|14041139|Sequence 7067 from Patent EP1108790
Length = 349980 (1 .. 349980)
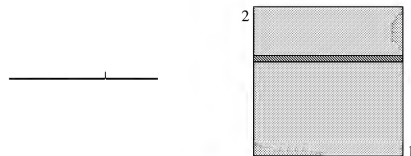
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

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 Score = 1656 bits (861), Expect = 0.0
 Identities = 861/861 (100%), Gaps = 0/861 (0%)
 Strand=Plus/Minus

Query  1       GAGTTGGCCGATTACATCCCGGAACTAAAATCTGCGGACCCAAACCCGCTGGCAGTAGCC  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227662  GAGTTGGCCGATTACATCCCGGAACTAAAATCTGCGGACCCAAACCCGCTGGCAGTAGCC  227603

Query  61      CTGTGCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227602  CTGTGCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATG  227543

Query  121     CAAAGTATTTCCAAGCCATTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAG  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227542  CAAAGTATTTCCAAGCCATTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAG  227483

Query  181     GTCTCTGCATCCGTGGCCTTGGAGCCCTCCGGTGAGGCCTTCAACGAACTTTCCCTCGAC  240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227482  GTCTCTGCATCCGTGGCCTTGGAGCCCTCCGGTGAGGCCTTCAACGAACTTTCCCTCGAC  227423

Query  241     GGCGAAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGATCGCCATCAACCAGCTG  300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  227422  GGCGAAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGATCGCCATCAACCAGCTG  227363

Query    301  ATCAACGGCTCCGATTCCACCGTGGAAGACCGCGTGGAAAAAATCCGACACTACTTCTCT  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227362  ATCAACGGCTCCGATTCCACCGTGGAAGACCGCGTGGAAAAAATCCGACACTACTTCTCT  227303

Query    361  GAACTTGCTGGACGCGAACTCACCATCGACCGCGTGCTTGCCGAATCCGAACTCGCCGGC  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227302  GAACTTGCTGGACGCGAACTCACCATCGACCGCGTGCTTGCCGAATCCGAACTCGCCGGC  227243

Query    421  GCCGACCGCAACCTCTCCATCGCCCACATGCTGCGCAATTACGGCGTCATCGAAGACGAA  480
              ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  227242  GCCGACCGCAACCTCTCCATCGCCCACATGCTGCGCAATTACGGCGTCATCGAAGACGAA  227183

Query    481  GCCCACGACGCCGTCCTCAGCTACACGCTGCAATGCGCCATCAAAGTAACCACGCGCGAC  540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227182  GCCCACGACGCCGTCCTCAGCTACACGCTGCAATGCGCCATCAAAGTAACCACGCGCGAC  227123

Query    541  CTCGCAGTCATGACCGCCACGCTCGCCGCCGGCGGCACACACCCAATTACCGGCAAGAAG  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227122  CTCGCAGTCATGACCGCCACGCTCGCCGCCGGCGGCACACACCCAATTACCGGCAAGAAG  227063

Query    601  CTTCTCGACGCCCGCGTCTGCCGCCTCACCCTCTCCGTCATGGCTTCAGCAGGCATGTAC  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227062  CTTCTCGACGCCCGCGTCTGCCGCCTCACCCTCTCCGTCATGGCTTCAGCAGGCATGTAC  227003

Query    661  GACGAGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGC  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  227002  GACGAGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGC  226943

Query    721  GGACTCATCGGCATTCTGCCCAGGTCAGCTGGGCATCGCCACATTTTCCCCACGCCTGAAC  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  226942  GGACTCATCGGCATTCTGCCCAGGTCAGCTGGGCATCGCCACATTTTCCCCACGCCTGAAC  226883

Query    781  CCCAAAGGCAACAGCGTGCGCGGCGTAAAAATATTCAAACAGCTTTCCGACGACATGGGC  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  226882  CCCAAAGGCAACAGCGTGCGCGGCGTAAAAATATTCAAACAGCTTTCCGACGACATGGGC  226823

Query    841  CTCCACCTCATGTCCACCGAG  861
              |||||||||||||||||||||
Sbjct  226822  CTCCACCTCATGTCCACCGAG  226802
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CPU time:      0.05 user secs.      0.05 sys. secs      0.10 total secs.
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